

04/15

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	1267.5	14.5	19938	6	ABP76680	Abp76680 Streptomy
c	2	1132	12.9	19938	6	ABP76679	Abp76679 Streptomy
	3	1113.5	12.1	19938	6	ABP76679	Abp76679 Streptomy
c	4	1107.5	12.7	19938	6	ABP76682	Abp76682 Streptomy
	5	1081.5	11.7	1953	6	AAE36881	Aae36881 Nephila m
c	6	1075	12.3	19938	6	ABP76681	Abp76681 Streptomy
c	7	1018.5	11.6	2294	7	ABO68485	Abo68485 Pseudomon
c	8	1013	11.6	1706	7	ABO83014	Abo83014 Pseudomon
	9	996.5	10.8	19938	6	ABP76680	Abp76680 Streptomy
c	10	995	11.4	1071	7	ADF94310	Adf94310 Human col
c	11	980.5	11.2	1064	2	AAR93254	Aar93254 Collagen-
c	12	980.5	11.2	1064	2	AAW57652	Aaw57652 Collagen-
c	13	980.5	11.2	1065	2	AAR37741	Aar37741 Collagen-
c	14	970.5	11.1	19938	6	ABB98398	Abb98398 Streptomy
	15	958.5	10.4	19938	6	ABB98398	Abb98398 Streptomy
	16	913.5	9.9	19938	6	ABP76681	Abp76681 Streptomy

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%									
Result		Query									
No.	Score	Match	Length	DB	ID	Description					
1	4826	100.0	4826	6	AR560982	AR560982 Sequence					
2	4824.4	100.0	4826	1	AY032926	AY032926 Streptomy					
3	1133	23.5	277000	1	SC0939109	AL939109 Streptomy					
c 4	1096.4	22.7	299925	1	AP005048	AP005048 Streptomy					
c 5	528	10.9	302007	1	SC0939132	AL939132 Streptomy					
c 6	331.8	6.9	3030	8	VCA429230	AJ429230 Volvox ca					
7	314.4	6.5	167254	9	CNS05TDS	AL357093 Human chr					
c 8	282.6	5.9	110000	1	AE000516_27	Continuation (28 o					
c 9	282.6	5.9	346051	1	BX842580	BX842580 Mycobacte					

12: geneseqn2004as:*
 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	ID	
	1	4826	100.0	4826	13 ADR31451	Adr31451 Streptomy
	2	4822.8	99.9	4826	8 ABX93509	Abx93509 DNA fragm
	3	294.4	6.1	114955	2 AAX53491	Aax53491 Human ade
c	4	282.6	5.9	110000	4 AAI99682_27	Continuation (28 o
c	5	282.6	5.9	110000	4 AAI99682_28	Continuation (29 o
c	6	282.6	5.9	110000	4 AAI99683_27	Continuation (28 o
c	7	271.8	5.6	114955	2 AAX53491	Aax53491 Human ade
	8	262.6	5.4	110000	4 AAI99683_39	Continuation (40 o
	9	260.4	5.4	110000	4 AAI99682_39	Continuation (40 o
c	10	257.4	5.3	2543	12 ACH87341	Ach87341 Human gen
c	11	257	5.3	110000	4 AAI99683_06	Continuation (7 of
	12	255.4	5.3	3921	8 ACA40351	Aca40351 Prokaryot
c	13	255.4	5.3	110000	4 AAI99682_06	Continuation (7 of
c	14	253	5.2	110000	4 AAI99683_39	Continuation (40 o
c	15	242.2	5.0	110000	4 AAI99682_39	Continuation (40 o
c	16	241.2	5.0	110000	4 AAI99682_37	Continuation (38 o
	17	239.6	5.0	110000	4 AAI99682_12	Continuation (13 o

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	4826	100.0	4826	4	US-09-772-304A-1	Sequence 1, Appli
c	2	282.6	5.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	3	282.6	5.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	4	262.6	5.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	5	260.4	5.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	6	188.2	3.9	6192	2	US-08-479-537A-1	Sequence 1, Appli
c	7	188.2	3.9	6192	3	US-09-083-116-1	Sequence 1, Appli
c	8	188.2	3.9	6192	3	US-09-134-916A-1	Sequence 1, Appli
c	9	188.2	3.9	6449	2	US-08-479-537A-4	Sequence 4, Appli
c	10	188.2	3.9	6449	3	US-09-083-116-4	Sequence 4, Appli
c	11	188.2	3.9	6449	3	US-09-134-916A-4	Sequence 4, Appli
	12	188	3.9	2457	4	US-09-863-859-21	Sequence 21, Appl
	13	188	3.9	4881	4	US-09-863-859-23	Sequence 23, Appl
	14	180	3.7	8438	1	US-07-945-283-1	Sequence 1, Appli

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query					Description
No.	Score	Match	Length	DB	ID		
c 1	280	5.8	2041	9	AG363808	AG363808 Mus muscu	
c 2	275.6	5.7	1695	8	CC290874	CC290874 CH261-172	
c 3	266.6	5.5	1674	9	CL078342	CL078342 CH216-149	
c 4	263.4	5.5	2332	9	AG363333	AG363333 Mus muscu	
5	262.2	5.4	1956	9	CG754548	CG754548 P050-1-A1	
6	261.6	5.4	1909	9	CL078604	CL078604 CH216-151	
7	259.4	5.4	1628	9	CG757066	CG757066 P052-2-A0	
8	258.2	5.4	1970	9	CG748837	CG748837 P042-4-E0	
9	253	5.2	1738	9	CG750956	CG750956 P045-2-H0	
c 10	251.6	5.2	2198	9	AG332729	AG332729 Mus muscu	
11	251	5.2	1839	9	CG747711	CG747711 P041-2-E0	
c 12	248.4	5.1	1788	8	CC320563	CC320563 TAM32-34P	
13	247.4	5.1	1793	9	CG754612	CG754612 P050-1-D0	

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query						Description
	No.	Score	Match	Length	DB	ID	
c	1	863.5	9.9	1188	2	S49915	extensin-like prot
c	2	841	9.6	924	2	S27923	gene LF3 protein -
	3	829	9.0	1660	2	A70869	hypothetical glyci
c	4	822	9.4	4776	2	E95206	cell wall surface
	5	800	8.7	1489	2	D70807	hypothetical glyci
	6	795	8.6	2639	2	T31328	fibroin - Chinese
	7	791.5	8.6	1381	2	E70806	hypothetical glyci
	8	791	8.6	1901	2	F70806	hypothetical glyci
	9	781.5	8.5	1079	2	B70807	hypothetical glyci
	10	777.5	8.4	1306	2	A70934	hypothetical glyci
	11	776.5	8.4	1329	2	E70917	hypothetical glyci
c	12	776.5	8.9	1344	1	A35175	mucin 1 precursor,
	13	775	8.4	1466	1	CGHU7L	collagen alpha 1(I
	14	774.5	8.4	13288	2	T03099	mucin, submaxillar
	15	753	8.2	2944	2	A54849	collagen alpha 1(V

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	4169	45.2	813	2	Q8GFF3	Q8gff3 streptomyce
c	2	3203	36.6	579	2	Q8GFF2	Q8gff2 streptomyce
	3	1795	19.5	368	2	Q8GFF1	Q8gff1 streptomyce
	4	1629	17.7	796	2	Q827V3	Q827v3 streptomyce
	5	1509	16.4	818	2	Q9F3E4	Q9f3e4 streptomyce
c	6	1351	15.4	263	2	Q8GFE8	Q8gfe8 streptomyce
c	7	1255	14.3	245	2	Q8GFF0	Q8gff0 streptomyce
c	8	1133.5	13.0	3409	2	Q6SSE6	Q6sse6 chlamydomon
c	9	1109.5	12.7	3889	2	Q6SSE8	Q6sse8 chlamydomon
	10	1081.5	11.7	1953	2	Q9BIT7	Q9bit7 nephila ina
c	11	1057.5	12.1	676	2	Q95JC9	Q95jc9 sus scrofa
c	12	1020	11.7	190	2	Q8GFE9	Q8gfe9 streptomyce
	13	930.5	10.1	1884	2	Q9NHW2	Q9nhw2 nephila ina
c	14	914.5	10.5	7524	2	Q6PZE0	Q6pze0 mus musculu
	15	891.5	9.7	2249	2	Q9NHW4	Q9nhw4 nephila cla
c	16	891	10.2	566	2	Q95JD1	Q95jd1 sus scrofa
c	17	863.5	9.9	1188	2	Q41805	Q41805 zea mays (m
c	18	841.5	9.6	2752	2	Q9UQ35	Q9uq35 homo sapien